Lab works on new model for HIV transmission and evolution

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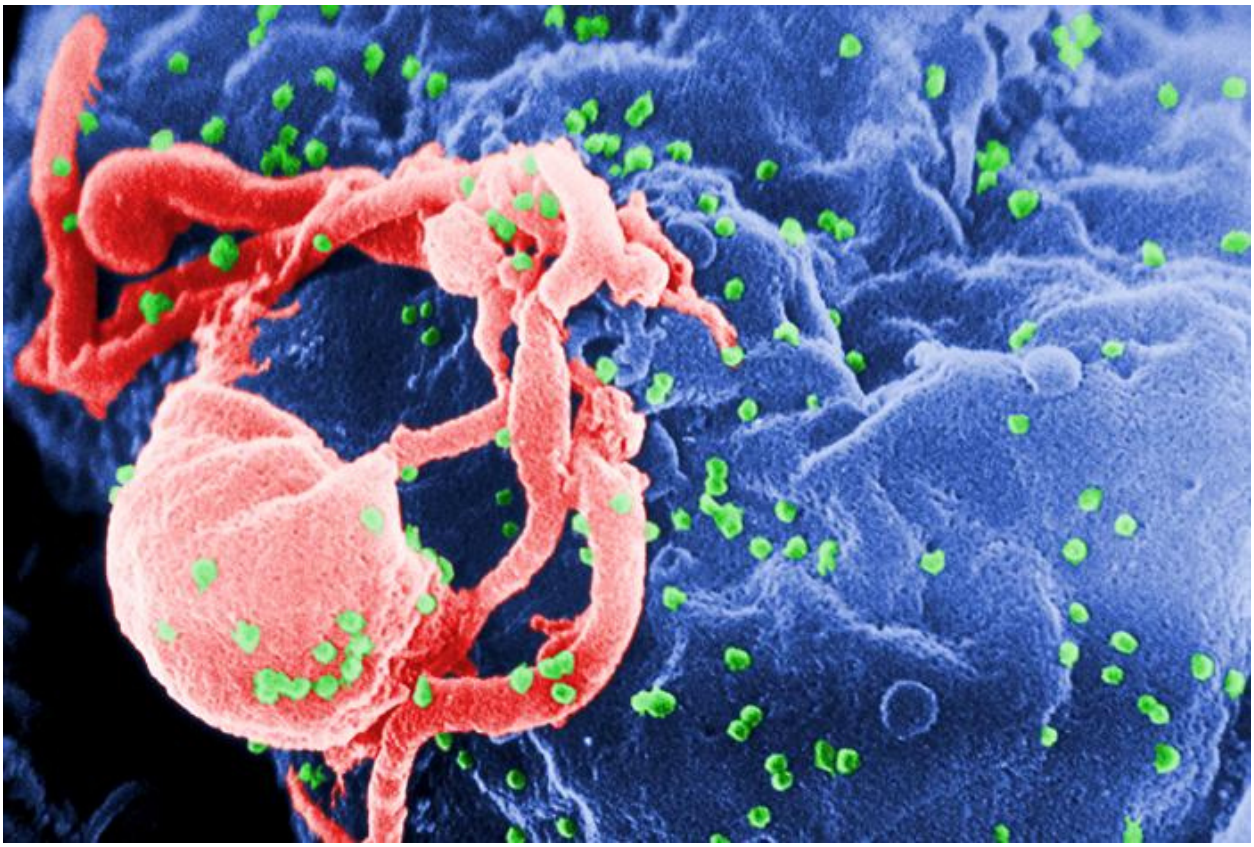

While the study of how disease spreads within populations (epidemiology) has been the subject of research for hundreds of years, new work taking place at the Laboratory is advancing how science views HIV transmission by adding in variables of viral evolution within its host (phylodynamics), said Thomas Leitner, the Lab's principal investigator for the project. The work could lead to better strategies on how to reduce the occurrence of HIV within populations around the world.

The hybrid model under development is leading to new insights about how HIV moves within populations by helping provide better estimates of how long people have been infected (and therefore have a higher probability of spreading the virus), the impacts of individuals social networks (including IV drug use) and adds to it the field of phylodynamics, or consideration of how the virus evolves over time. The

simulations can contain as many as several thousand people at a time with a variety of interconnections between them.

The researchers have shown that different populations see different amounts of viral changes. For instance, while the virus can spread quickly within a network that shares needles for drug injections, the virus itself shows little diversification. In other cases, the virus might spread more slowly but tends to mutate more rapidly within the same period of time.

These results have implications for public-health interventions that could help slow the spread of the disease. The Lab scientists continue to refine the model and will make the software and their results available to other researchers in other countries.

Researchers include Ruy M. Ribeiro and Ethan Romero-Severson with the Lab; Jan Albert, with the Karolinska Institute and Karolinska University; and Frederik Graw and Helena Skar, formerly with the Lab. The National Institutes of Health funded the research.

To read the full press release, go here.